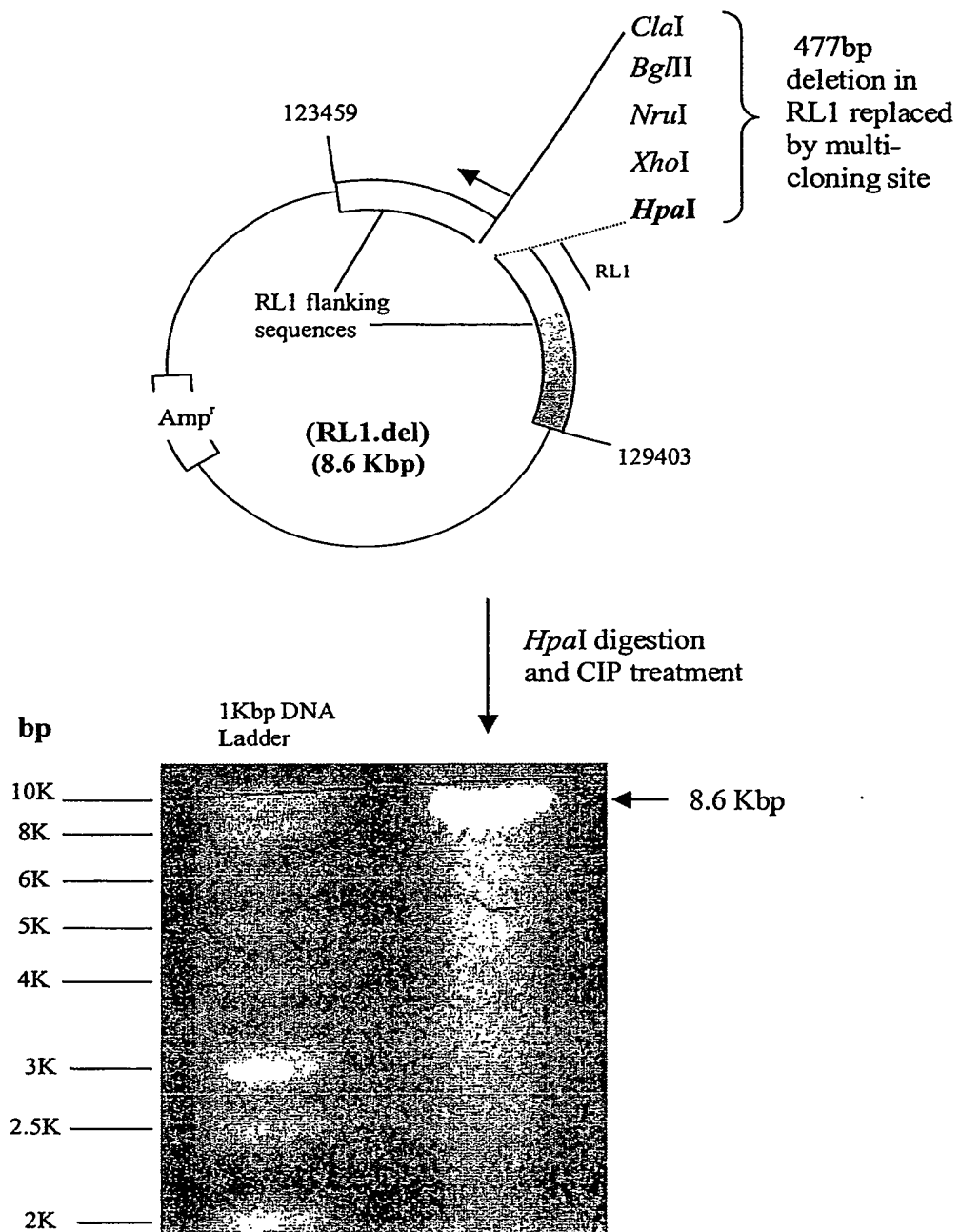


Figure 1

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**Figure 2**

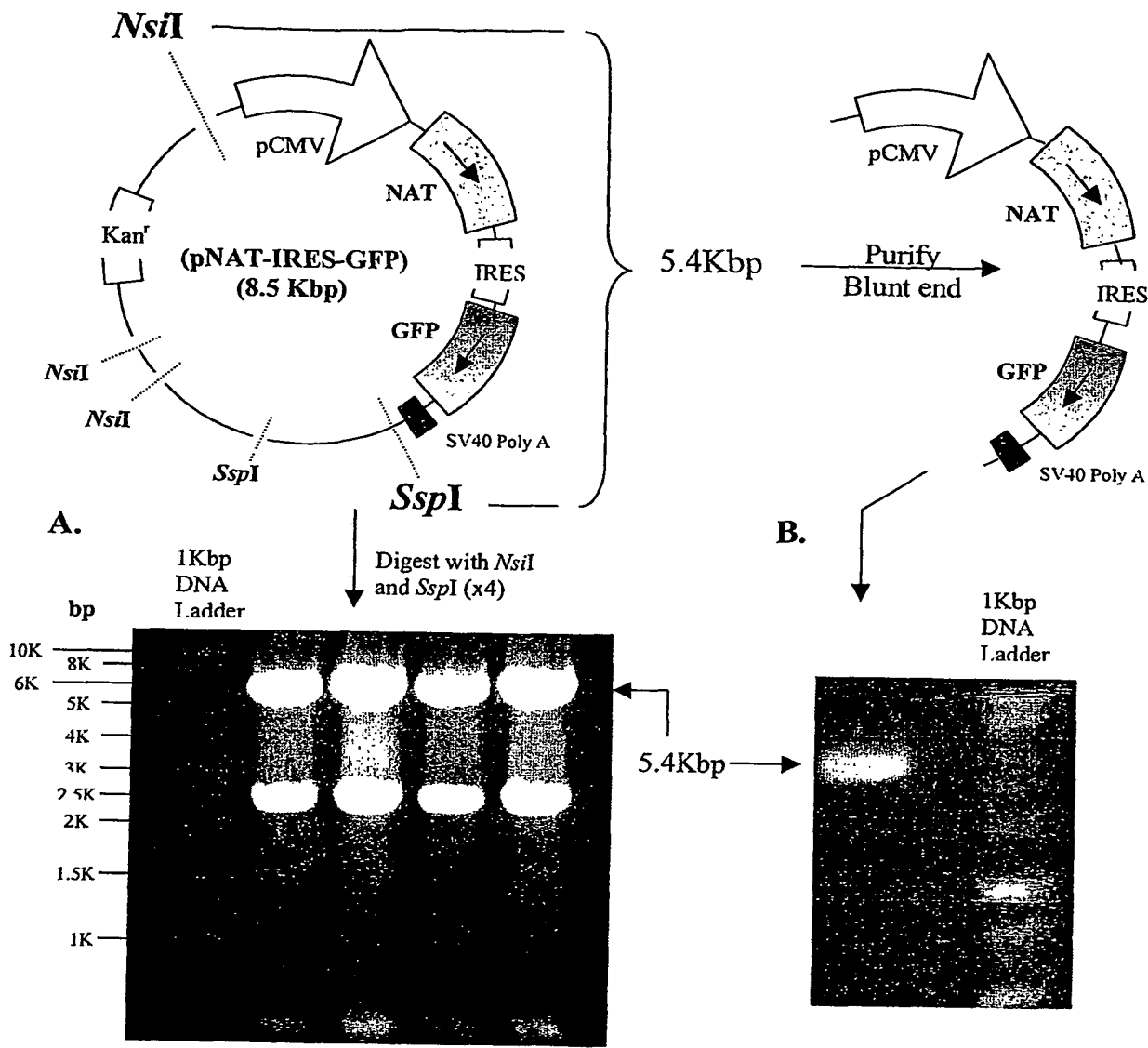


Figure 3

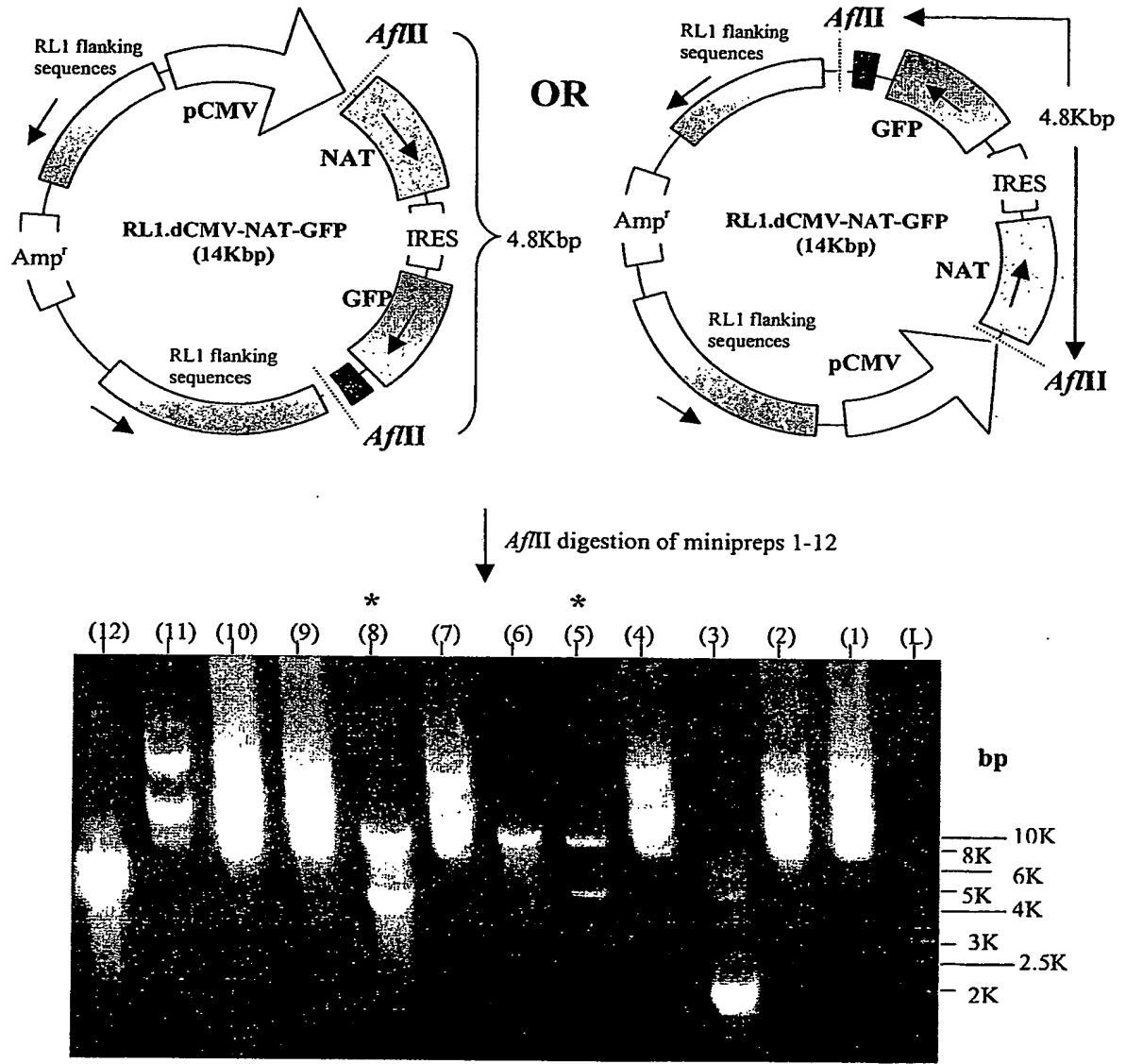
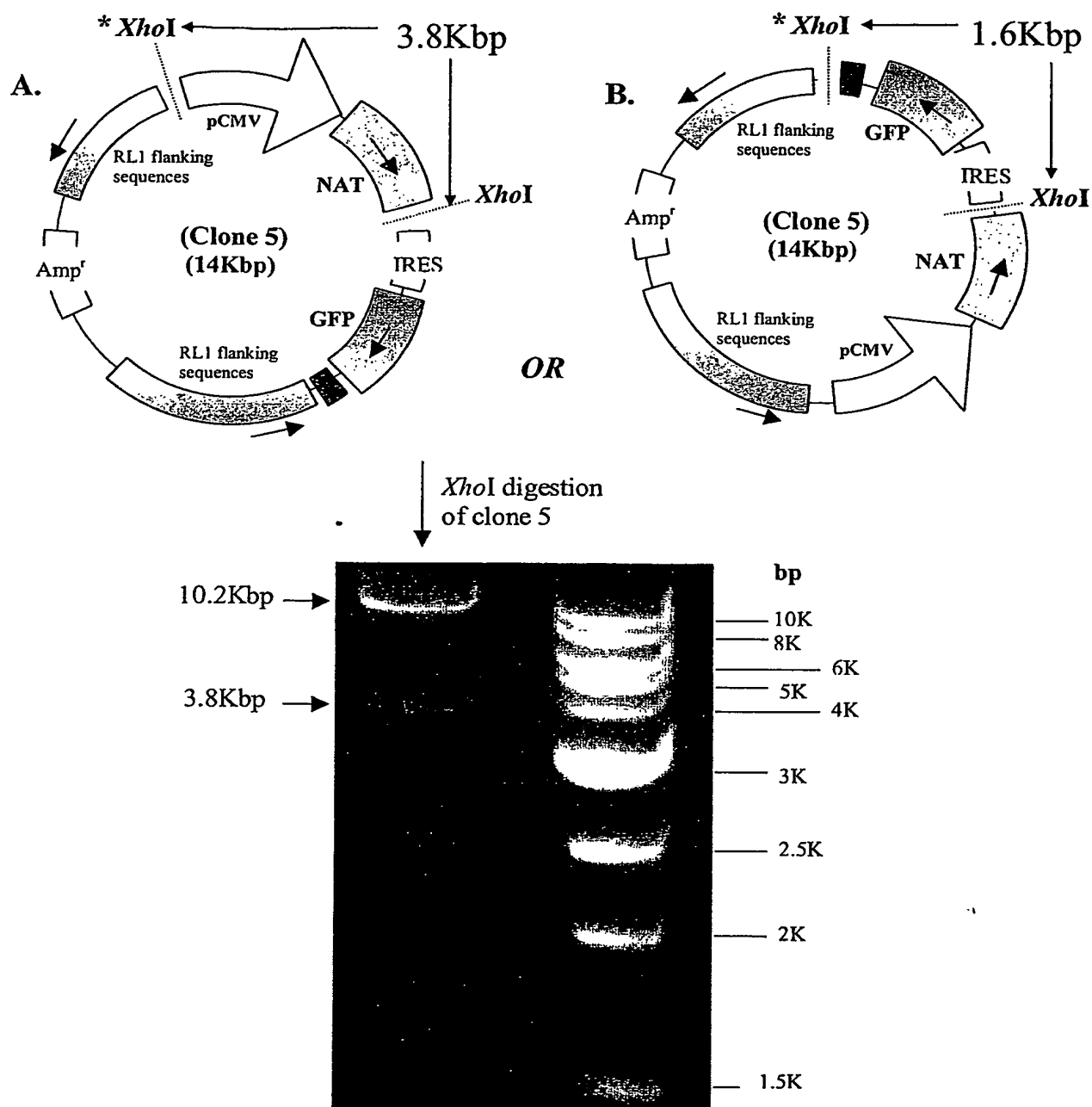


Figure 4

**Figure 5**

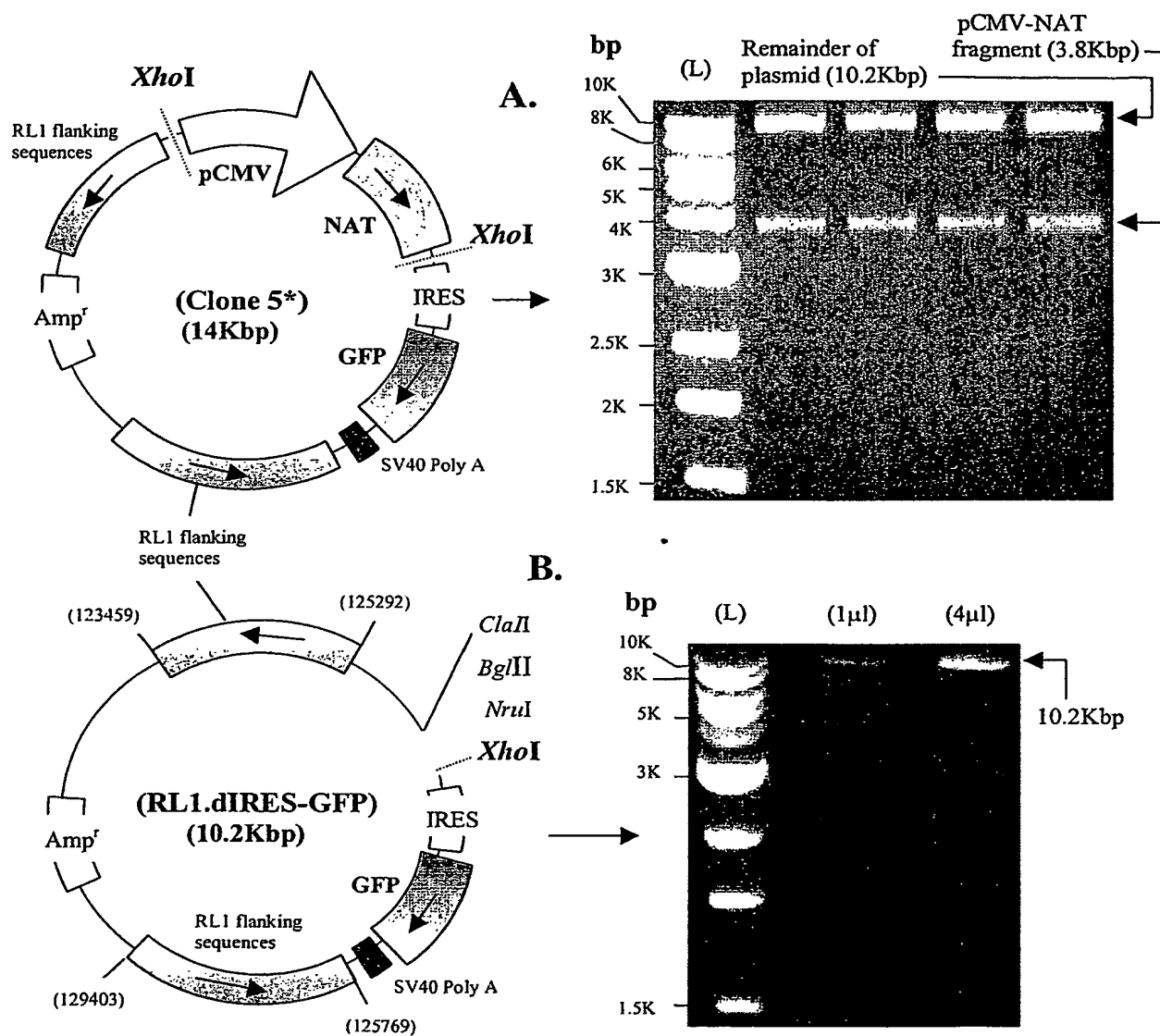


Figure 6

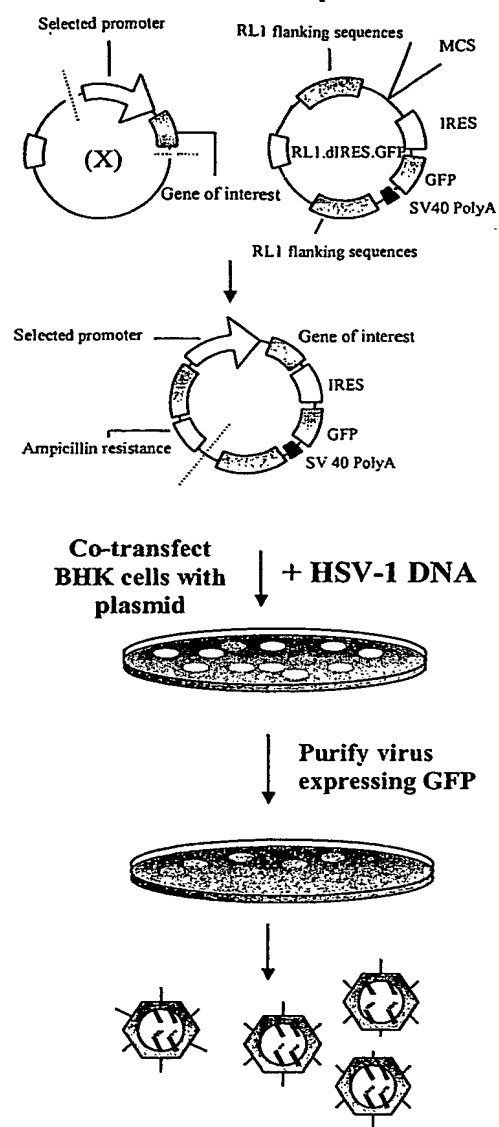


Figure 7

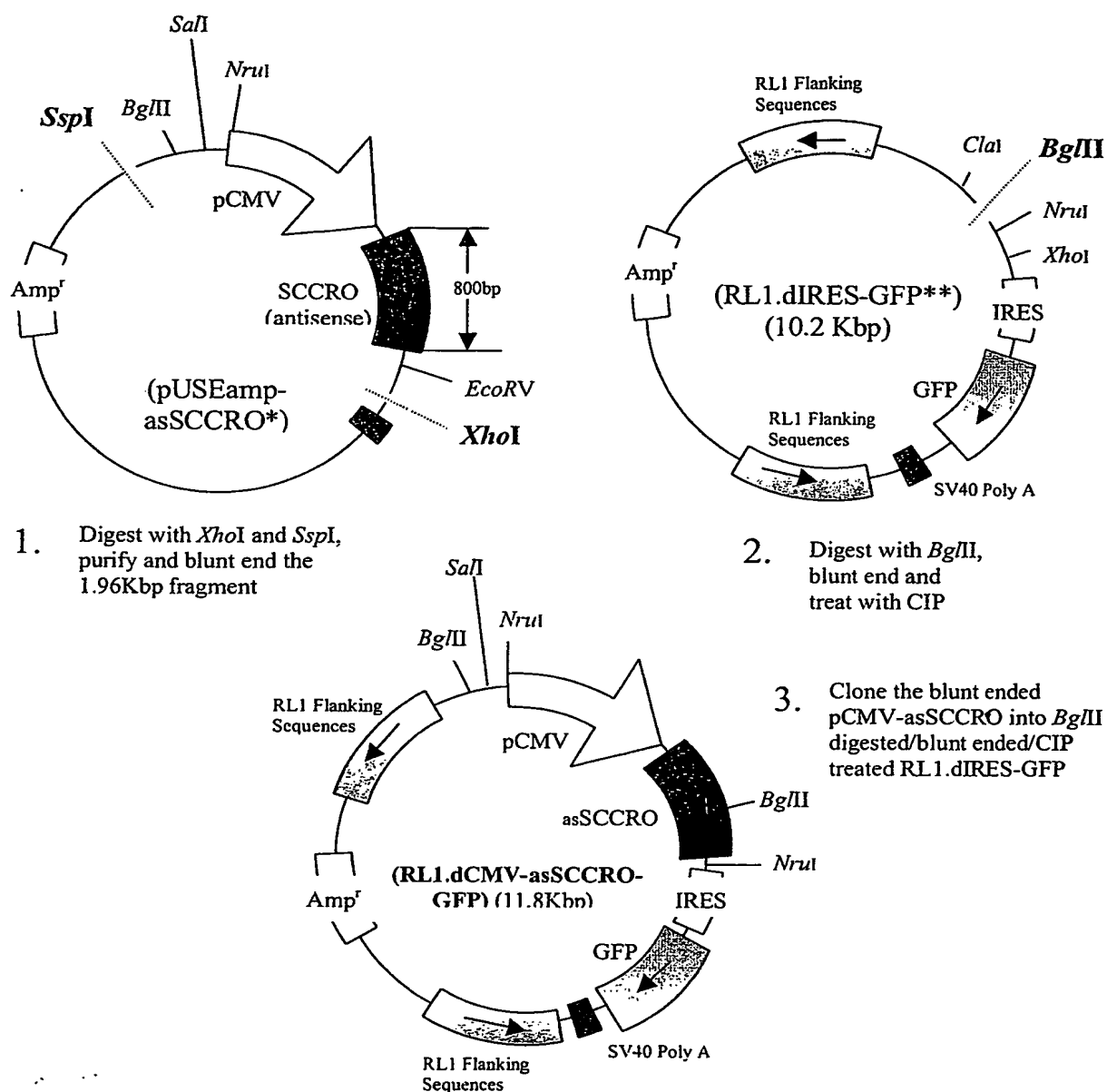
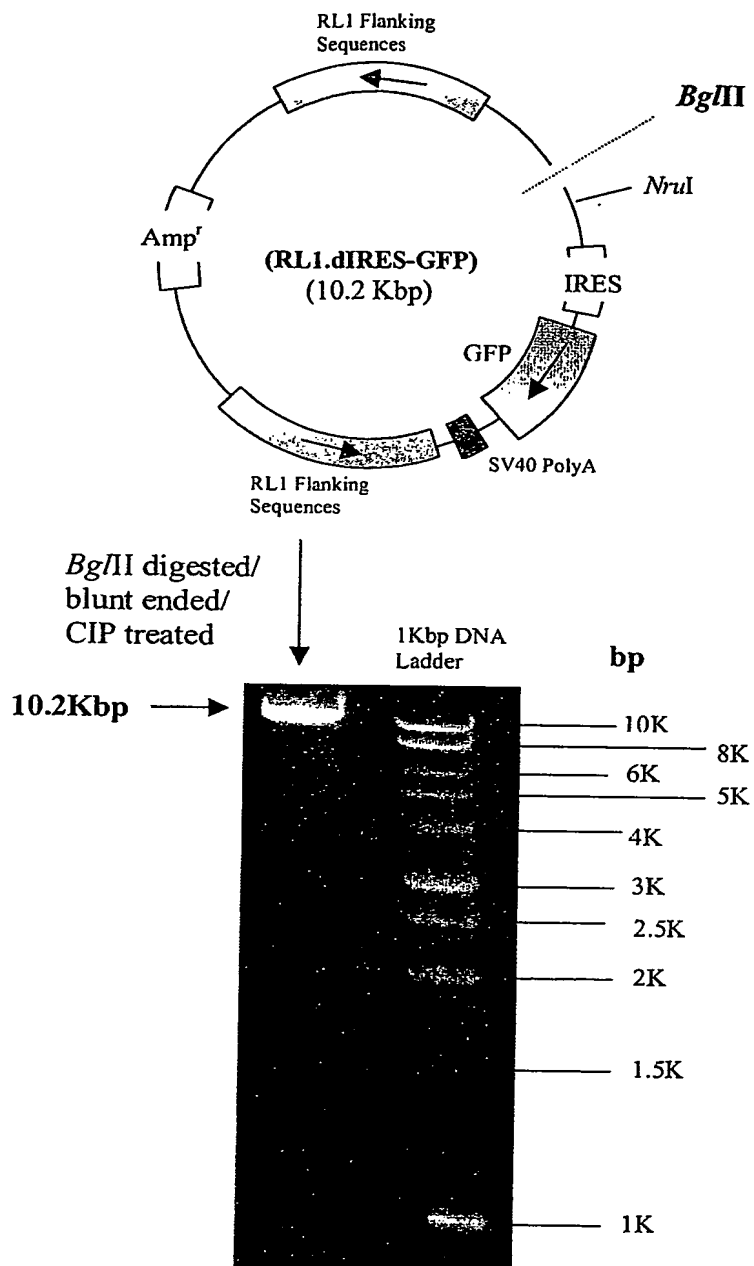


Figure 8

**Figure 9**

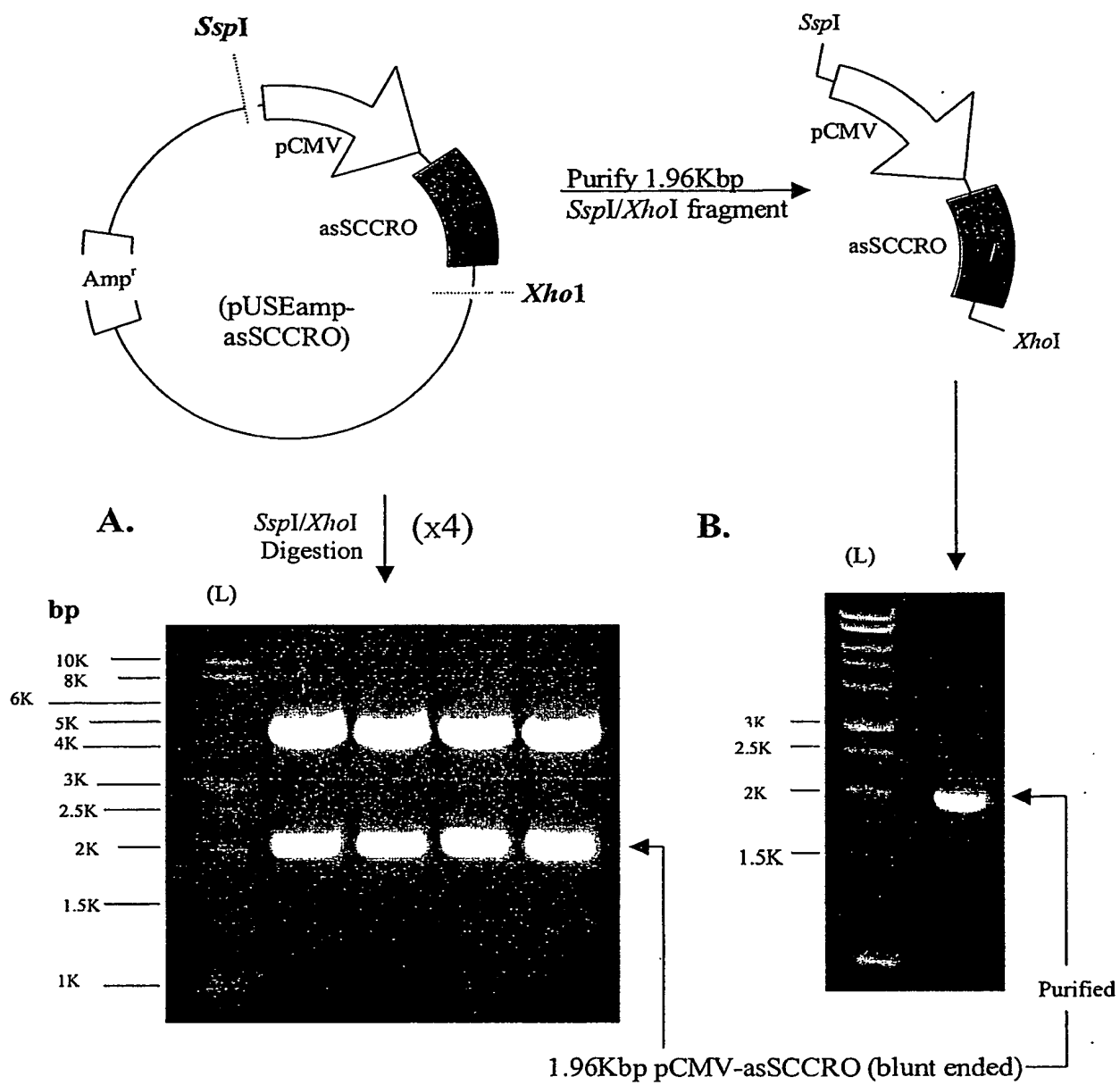


Figure 10

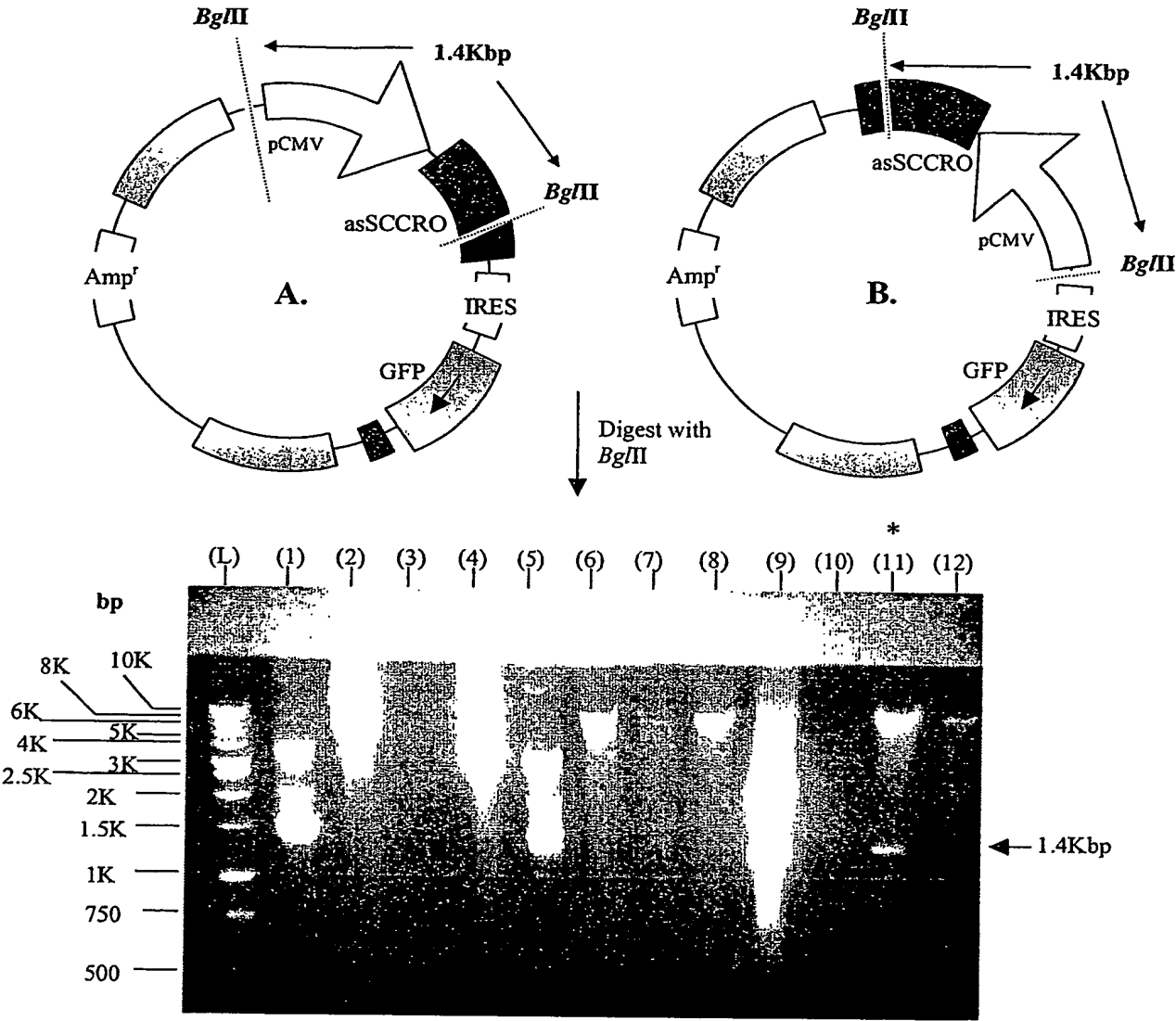


Figure 11

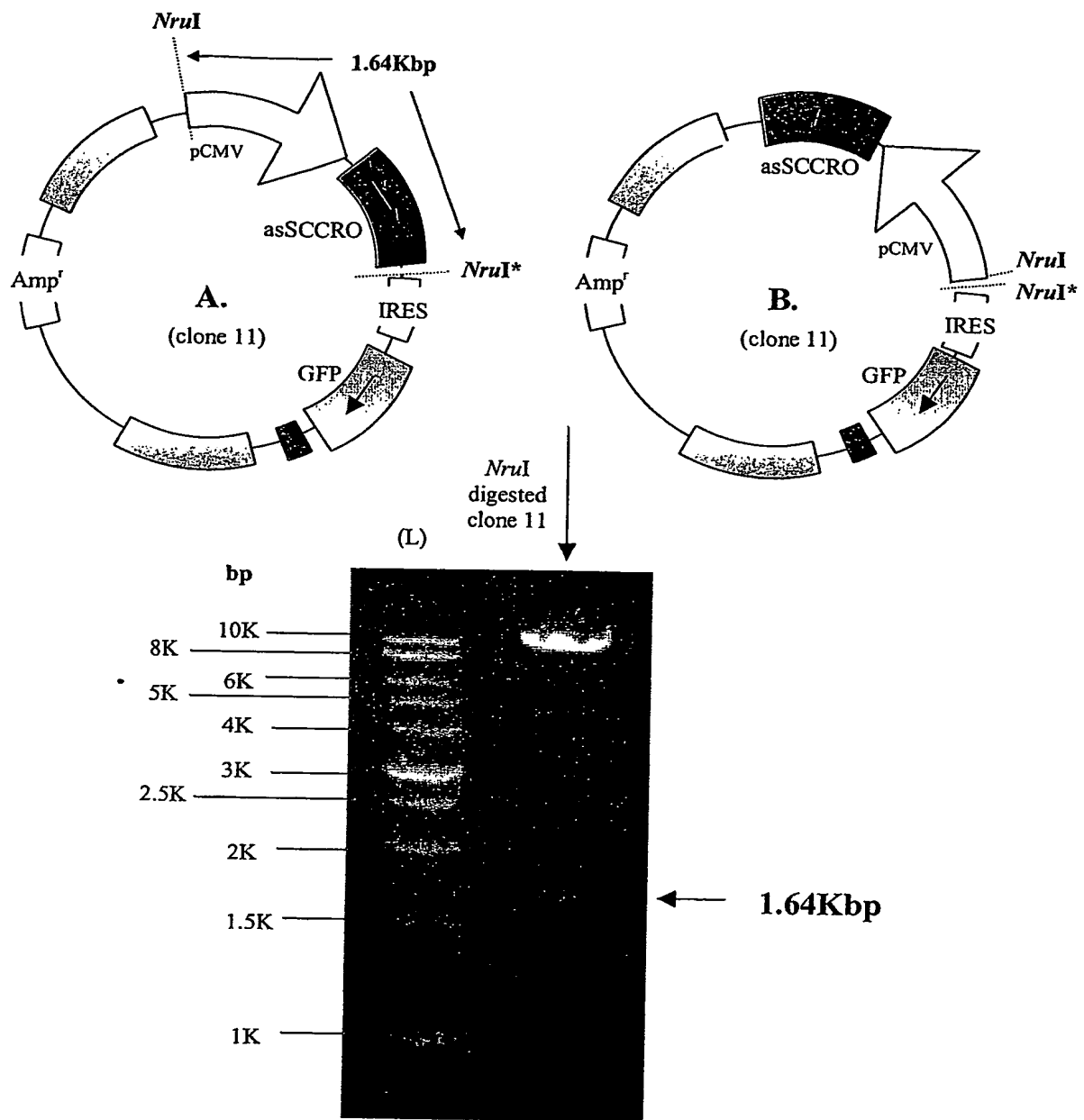
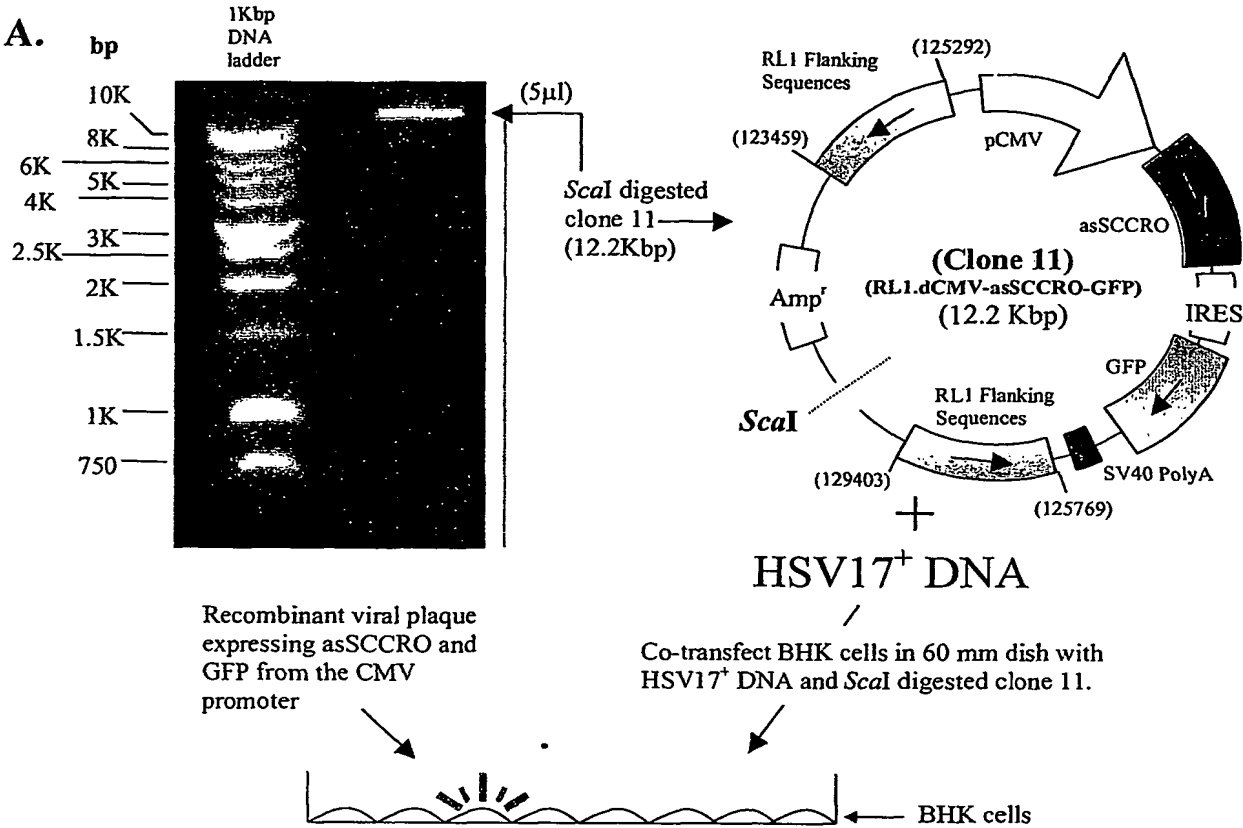


Figure 12



B.

HSV1716/CMV- asSCCRO/GFP Fraction	Titre
Combined	1.2×10^{10} pfu/ml

Figure 13

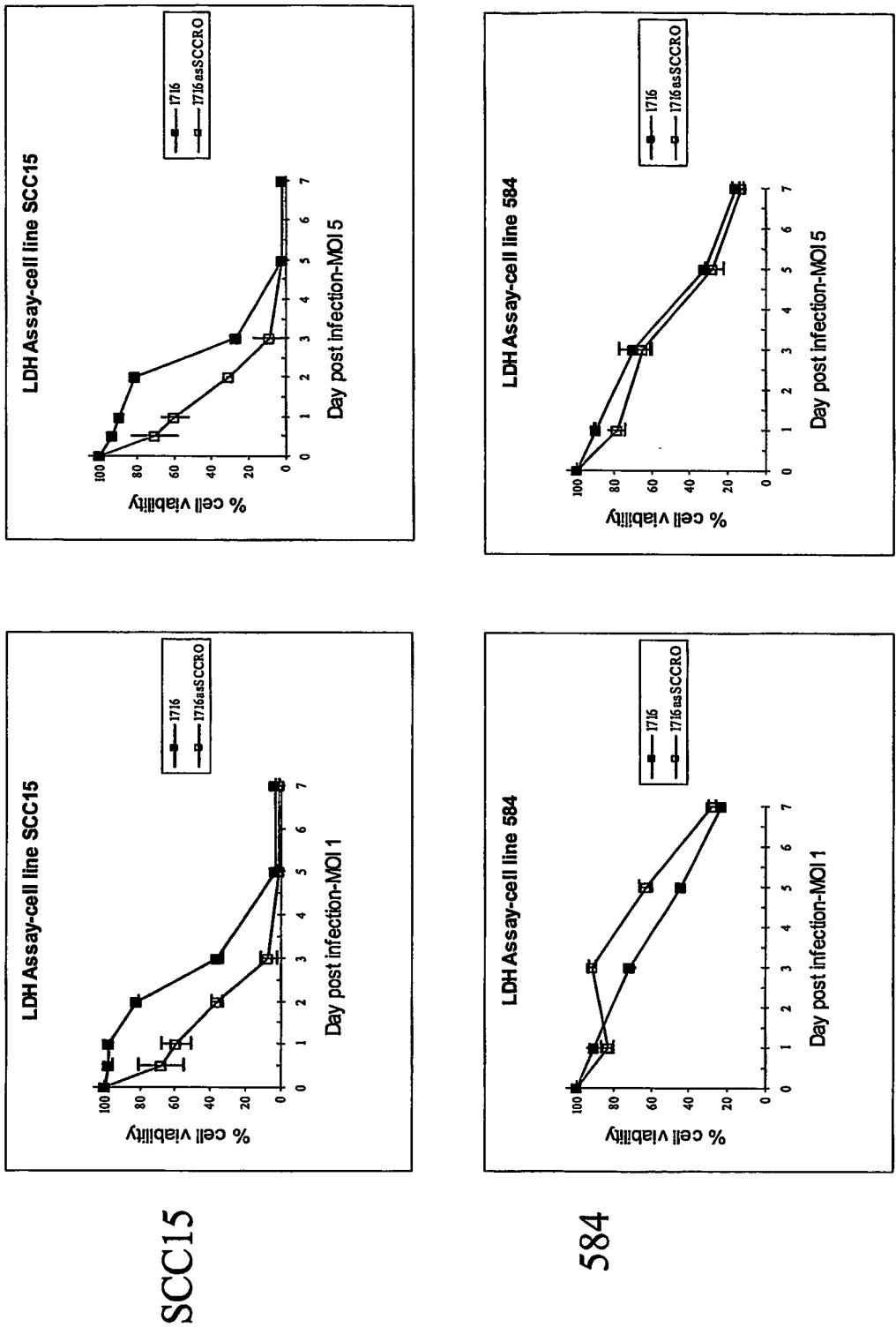


Figure 14

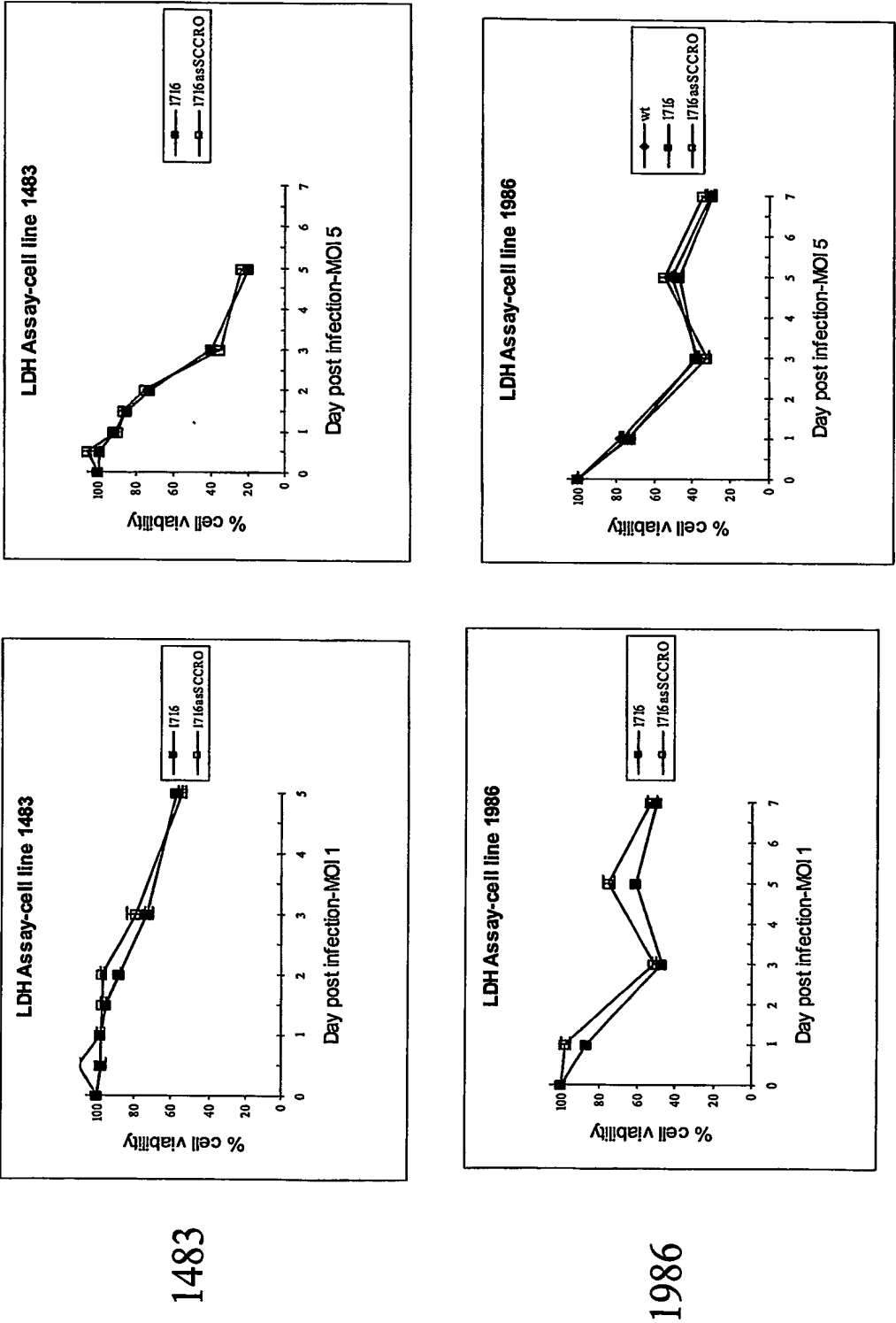
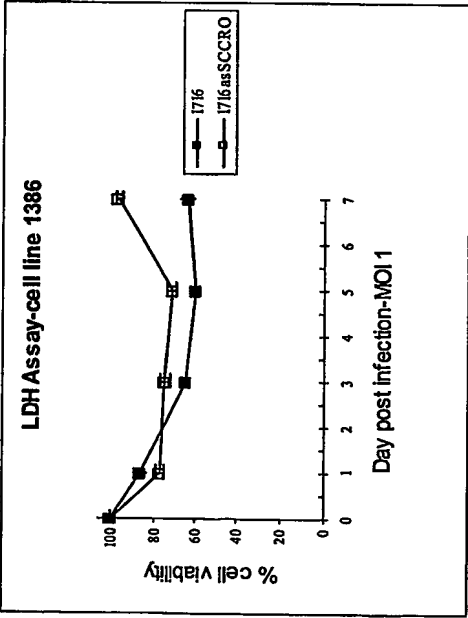
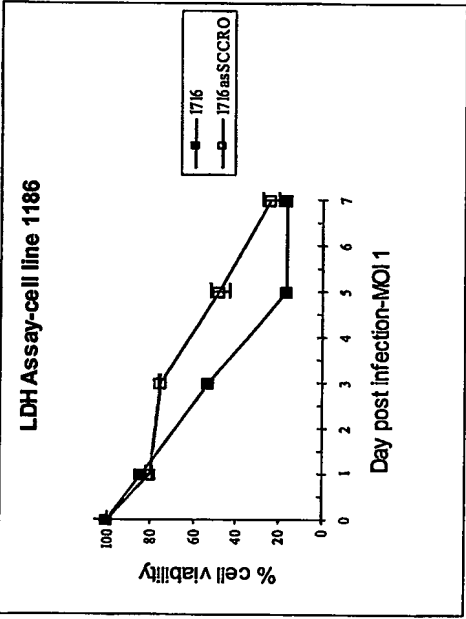
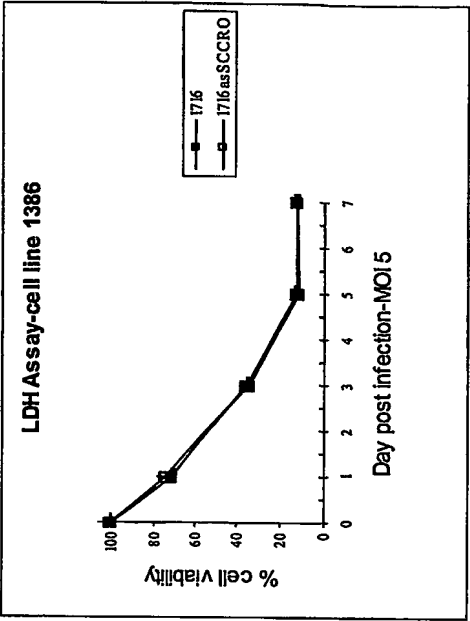
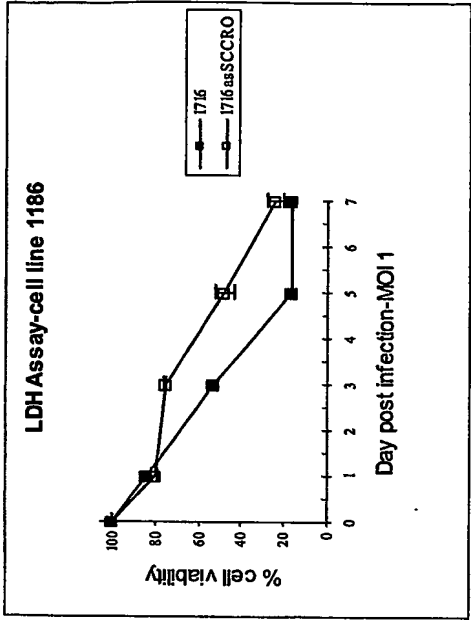


Figure 15



1186

1386

Figure 16

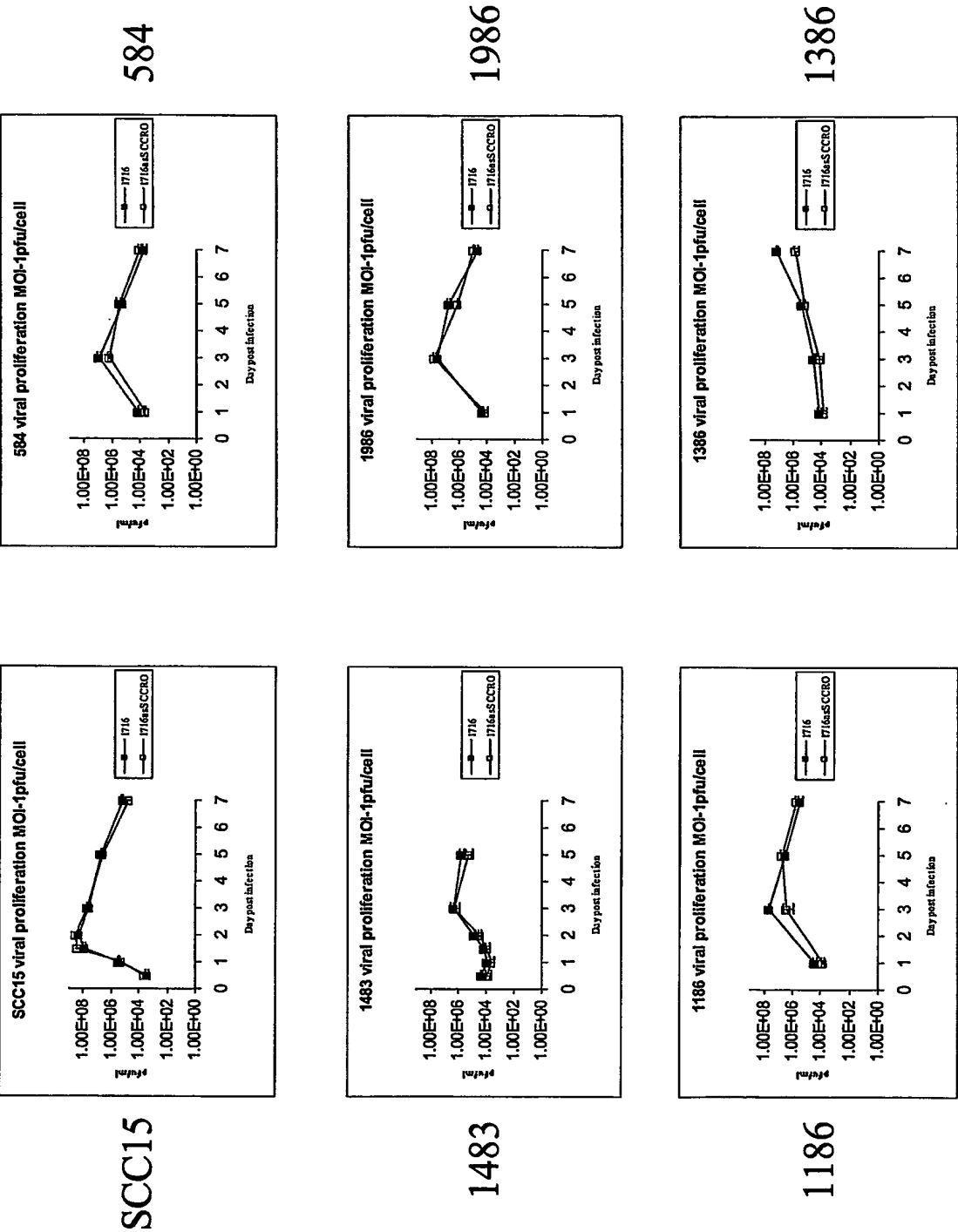


Figure 17

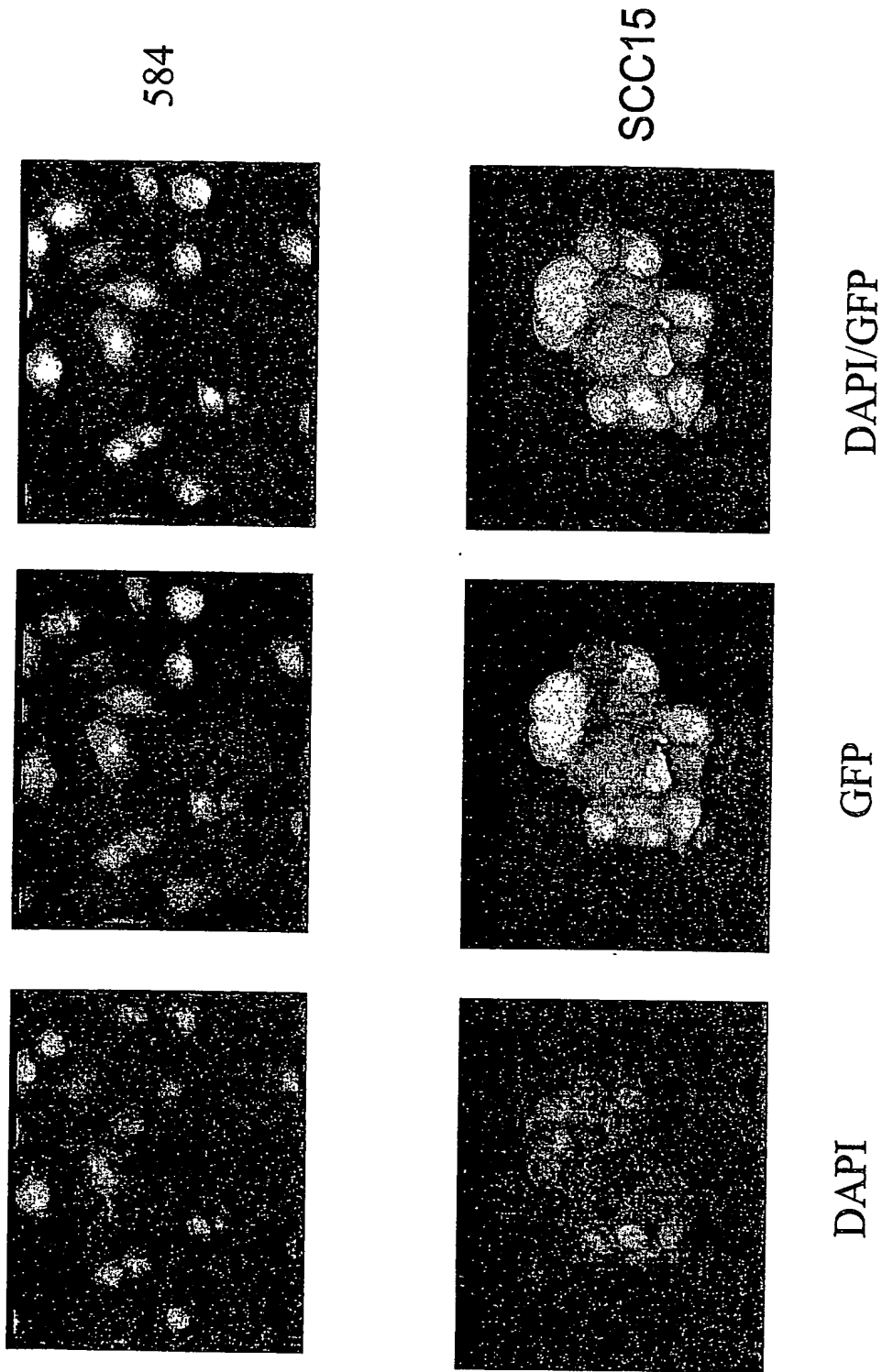


Figure 18

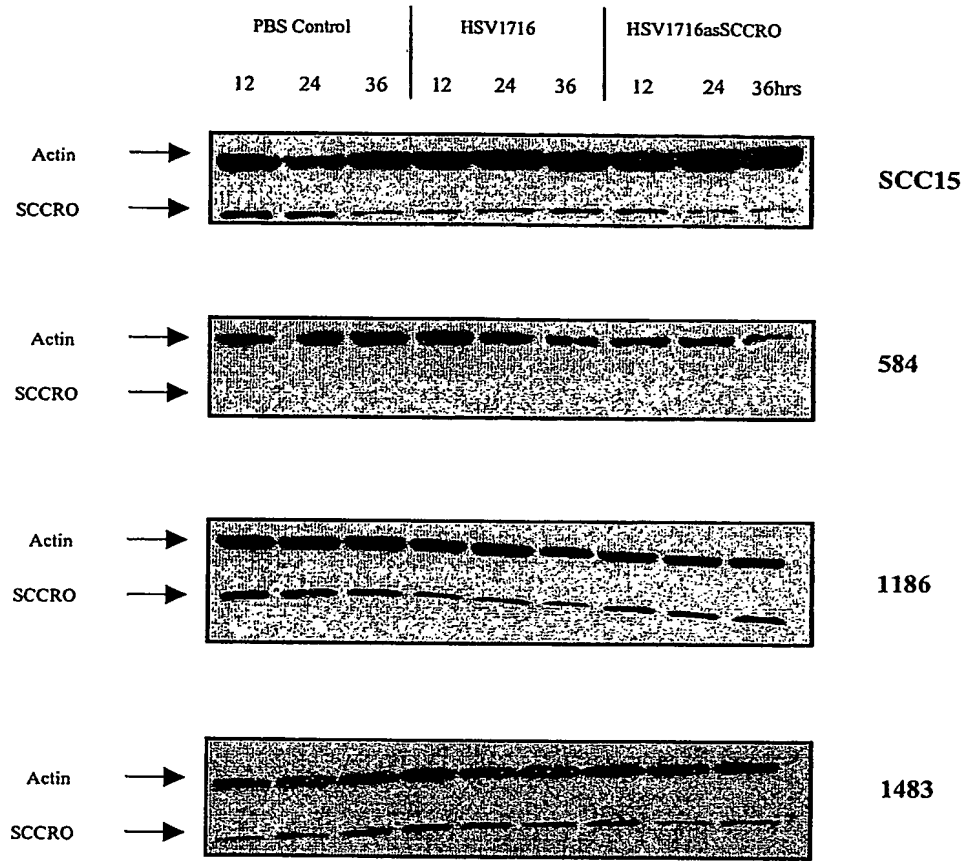
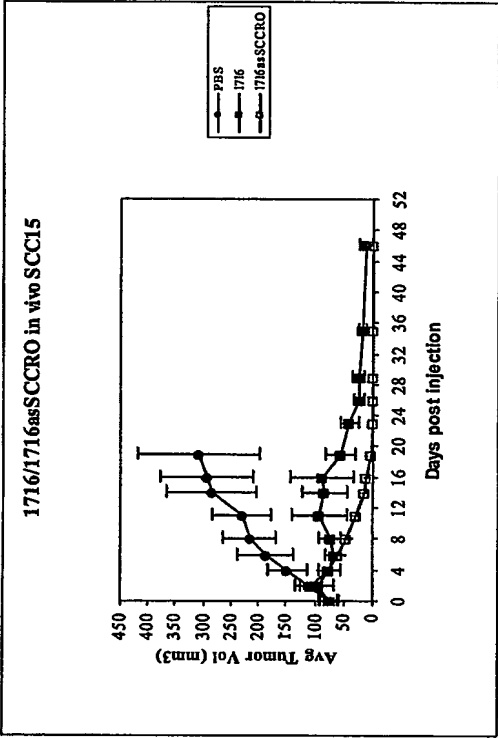


Figure 19

SCC15



584

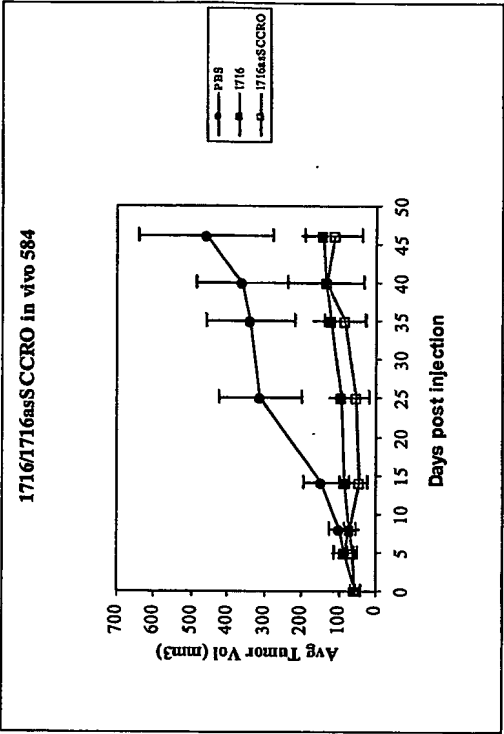


Figure 20

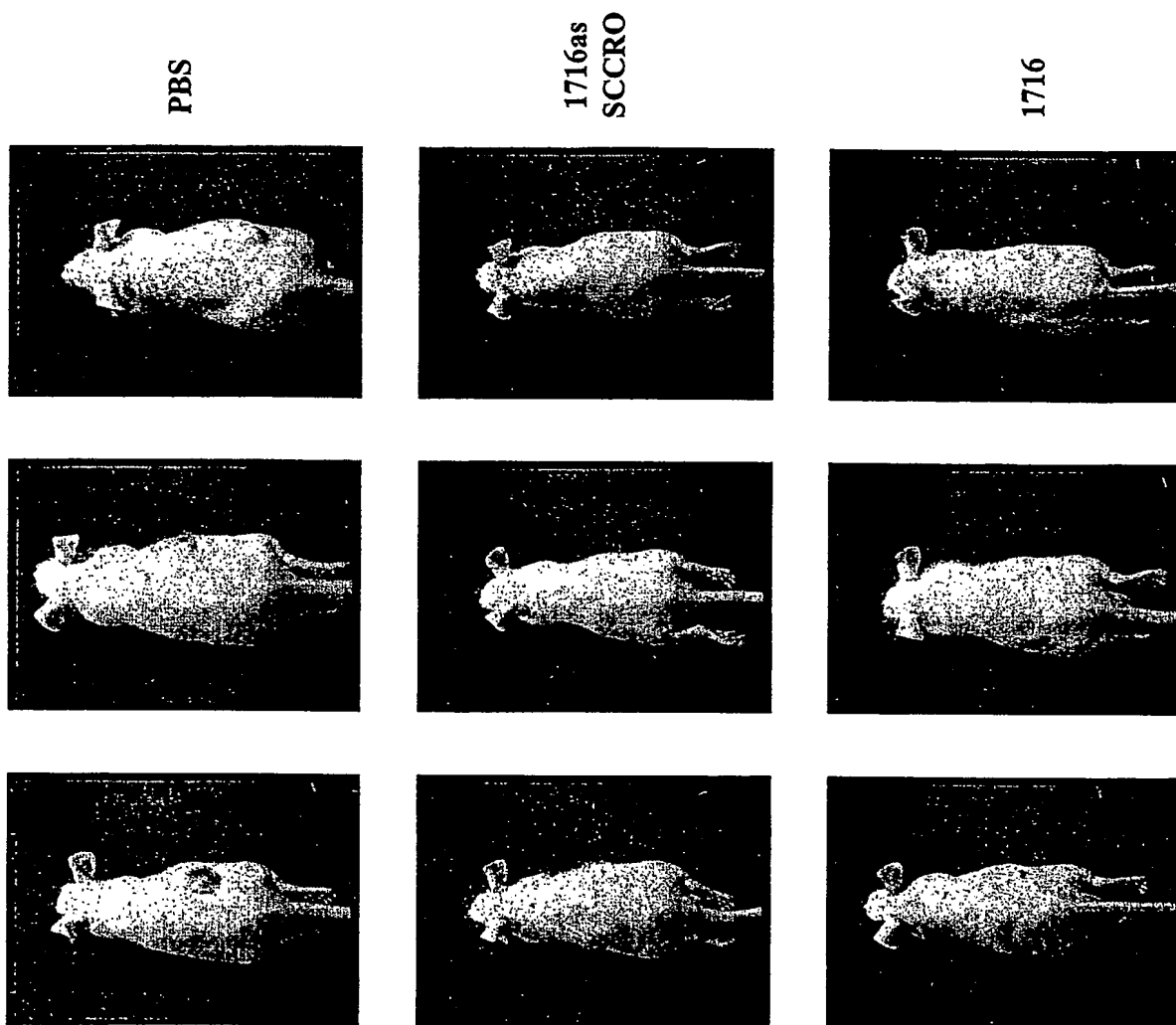


Figure 21

SEQ ID No. 01

cgcgcgtacat tcgctgagga gacggaggag gaggggagag gacggaggga caccaac atg 60
 Met
 1
 aac aag ttg aaa tca tcg cag aag gat ana gtc cgt cag ttt atg atc 108
 Asn Lys Leu Lys Ser Ser Gln Lys Asp Lys Val Arg Gln Phe Met Ile
 5 10 15
 ttc aca caa tct agt gaa aaa aca gca gta agt tgt ctt tct caa aat 156
 Phe Thr Gln Ser Ser Glu Lys Thr Ala Val Ser Cys Leu Ser Gln Asn
 20 25 30
 gac tgg aag tta gat gtt gca aca gat aat ttt ttc caa aat cct gaa 204
 Asp Trp Lys Leu Asp Val Ala Thr Asp Asn Phe Phe Gln Asn Pro Glu
 35 40 45
 ctt tat ata cga gag agt gta aaa gga tca ttg gac agg aag aag tta 252
 Leu Tyr Ile Arg Glu Ser Val Lys Gly Ser Leu Asp Arg Lys Lys Leu
 50 55 60 65
 gaa cag ctg tac aat aga tac aaa gac cct caa gat gag aat aaa att 300
 Glu Gln Leu Tyr Asn Arg Tyr Lys Asp Pro Gln Asp Glu Asn Lys Ile
 70 75 80
 gga ata gat ggc ata aag cag ttc tgt gat gac ctg gca ctc gat cca 348
 Gly Ile Asp Gly Ile Gln Gln Phe Cys Asp Asp Leu Ala Leu Asp Pro
 336
 gcc agc att agt gtg ttg att att gca tgg aag ttc aga gca gca aca
 Ala Ser Ile Ser Val Leu Ile Ile Ala Trp Lys Phe Arg Ala Ala Thr
 100 105 110
 cag tgc gag ttc tcc aaa cag gag ttc atg gat ggc atg aca gaa tta 444
 Gln Cys Glu Phe Ser Lys Gln Glu Phe Met Asp Gly Met Thr Glu Leu
 115 120 125
 gga tgt gac agc ata gaa aaa ata aag gcc cag ata ccc aag atg gaa 492
 Gly Cys Asp Ser Ile Glu Lys Leu Lys Ala Gln Ile Pro Lys Met Glu
 130 135 140 145
 caa gaa ttg aaa gaa cca gga cga ttt aag gat ttt taa cag ttt act 540
 Gln Glu Leu Lys Glu Pro Gly Arg Phe Lys Asp Phe Tyr Gln Phe Thr
 150 155 160
 ttt aat ttt gca aag aat cca gga caa aaa gga tta gat cta gaa atg 588
 Phe Asn Phe Ala Lys Asn Pro Gly Gln Lys Gly Leu Asp Leu Glu Met
 165 170 175
 gcc att gcc tac tgg aac tta gtg ctt aat gga aga ttt aaa ttc tta 636
 Ala Ile Ala Tyr Trp Asn Leu Val Leu Asn Gly Arg Phe Lys Phe Leu
 180 185 190
 gac tta tgg aat aaa ttt ttg ttg gaa cat cat aaa cga tca ata cca 684
 Asp Leu Trp Asn Lys Phe Leu Leu Glu His His Lys Arg Ser Ile Pro
 195 200 205
 aaa gac act tgg aat ctt ctt tta gac ttc agt acg atg att gca gat 732
 Lys Asp Thr Trp Asn Leu Leu Asp Phe Ser Thr Met Ile Ala Asp
 210 215 220 225
 gac atg tct aat tat gat gaa gaa gga gca tgg cct gtt ctt att gat 780
 Asp Met Ser Asn Tyr Asp Glu Glu Gly Ala Trp Pro Val Leu Ile Asp
 230 235 240
 gac ttt gtg gaa ttt gca cgc cct cna att gct ggg acn aza agt aca 828
 Asp Phe Val Glu Phe Ala Arg Pro Gln Ile Ala Gly Thr Lys Ser Thr
 245 250 255
 aca gtg tag aactaaagga acattataga atgtacatag tctgtacant 877
 Thr Val
 aactacaaca gaaattgca aagtaatttt atgtgggtg g 918

Figure 22a

SEQ ID No. 02

```

Met Asn Lys Leu Lys Ser Ser Gln Lys Asp Lys Val Arg Gln Phe Met
 1           5           10           15

Ile Phe Thr Gln Ser Ser Glu Lys Thr Ala Val Ser Cys Leu Ser Gln
 20           25           30

Asn Asp Trp Lys Leu Asp Val Ala Thr Asp Asn Phe Phe Gln Asn Pro
 35           40           45

Glu Leu Tyr Ile Arg Glu Ser Val Lys Gly Ser Leu Asp Arg Lys Lys
 50           55           60

Leu Glu Gln Leu Tyr Asn Arg Tyr Lys Asp Pro Gln Asp Glu Asn Lys
 65           70           75           80

Ile Gly Ile Asp Gly Ile Gln Gln Phe Cys Asp Asp Leu Ala Leu Asp
 85           90           95

Pro Ala Ser Ile Ser Val Leu Ile Ile Ala Trp Lys Phe Arg Ala Ala
100           105           110

Thr Gln Cys Glu Phe Ser Lys Gln Glu Phe Met Asp Gly Met Thr Glu
115           120           125

Leu Gly Cys Asp Ser Ile Glu Lys Leu Lys Ala Gln Ile Pro Lys Met
130           135           140

Glu Gln Glu Leu Lys Glu Pro Gly Arg Phe Lys Asp Phe Tyr Gln Phe
145           150           155           160

Thr Phe Asn Phe Ala Lys Asn Pro Gly Gln Lys Gly Leu Asp Leu Glu
165           170           175

Met Ala Ile Ala Tyr Trp Asn Leu Val Leu Asn Gly Arg Phe Lys Phe
180           185           190

Leu Asp Leu Trp Asn Lys Phe Leu Leu Glu His His Lys Arg Ser Ile
195           200           205

Pro Lys Asp Thr Trp Asn Leu Leu Leu Asp Phe Ser Thr Met Ile Ala
210           215           220

Asp Asp Met Ser Asn Tyr Asp Glu Glu Gly Ala Trp Pro Val Leu Ile
225           230           235           240

Asp Asp Phe Val Glu Phe Ala Arg Pro Gln Ile Ala Gly Thr Lys Ser
245           250           255

Thr Thr Val

```

Figure 22b

SEQ ID No.03

ctggaggaca caaac atg aac aag ttg aaa tca tgg cag aag gat aac gtt 91
 Met Asn Lys Leu Lys Ser Ser Gln Lys Asp Lys Val
 1 5 10

cgt aag ttt atg atc ttc aca caa tct agt gaa naa aca gca gta agt 99
 Arg Gln Phe Met Ile Phe Thr Gln Ser Ser Glu Lys Thr Ala Val Ser
 15 20 25

tgt att tct caa aat gac tgg aag tta gat gtt gca aca gat aat ttt 147
 Cys Leu Ser Gln Asn Asp Trp Lys Leu Asp Val Ala Thr Asp Asn Phe
 30 35 40

ttc caa aat cct gaa att tat ata cga gag agt gta aca gga tca ttg 195
 Phe Gln Asn Pro Glu Leu Tyr Ile Arg Glu Ser Val Lys Gly Ser Leu
 45 50 55 60

gac agg aag aag tta gaa cag ctg tac aat aga tac aca gac cct caa 243
 Asp Arg Lys Lys Phe Glu Gln Leu Tyr Asn Arg Tyr Lys Asp Pro Gln
 65 70 75

gat gag aat aca att gga ata gat ggc ata cag cag ttc tgt gat gac 291
 Asp Glu Asn Lys Ile Gly Ile Asp Gly Ile Gln Gln Phe Cys Asp Asp
 80 85 90

ctg gca ctc gat cca gcc agc att agt gtg ttg att att gag tgg aag 339
 Leu Ala Leu Asp Pro Ala Ser Ile Ser Val Leu Ile Ile Ala Trp Lys
 95 100 105

ttc aga gca gca aca cag tgc gag ttc tcc aca cag gag ttc atg gat 387
 Phe Arg Ala Ala Thr Gln Cys Glu Phe Ser Lys Gln Glu Phe Met Asp
 110 115 120

ggc atg aca gaa tta gga tgt gac agc aca gaa naa cta aag gcc cag 435
 Gly Met Thr Glu Leu Gly Cys Asp Ser Thr Glu Lys Leu Lys Ala Gln
 125 130 135 140

ata ccc aag atg gaa caa gaa ttg aaa gaa cca gga cga ttt aag gat 483
 Ile Pro Lys Met Glu Gln Glu Leu Lys Glu Pro Gly Arg Phe Lys Asp
 145 150 155

ttt tac cag ttt aot ttt aat ttt gaa aag aat aca gga caa aaa gga 531
 Phe Tyr Gln Phe Thr Phe Asn Phe Ala Lys Asn Pro Gly Gln Lys Gly
 160 165 170

tta gat cta gaa atg gcc att gcc tac tgg aac tta gtg ctt aat gga 579
 Leu Asp Leu Glu Met Ala Ile Ala Tyr Trp Asn Leu Val Leu Asn Gly
 175 180 185

aga ttt aga ctc tta gac tta tgg aat aca ttt ttg ttg gaa cat cat 627
 Arg Phe Arg Leu Leu Asp Leu Trp Asn Lys Phe Leu Leu Glu His His
 190 195 200

aca cga tca ata cca aca gac act tgg aat ctt ctt tta gac ttc agt 675
 Lys Arg Ser Ile Pro Lys Asp Thr Trp Asn Leu Leu Asp Phe Ser
 205 210 215 220

aag atg att gca gat gac atg tct aat tat gat gaa gaa gga gca tgg 723
 Thr Met Ile Ala Asp Asp Met Ser Asn Tyr Asp Glu Glu Gly Ala Trp
 225 230 235

cct gtt ctt att gat gac ttt gtg gaa ttt gca cgc cct caa att gat 771
 Pro Val Leu Ile Asp Asp Phe Val Glu Phe Ala Arg Pro Gln Ile Ala
 240 245 250

ggg aca aaa agt aca aca gtg tag cactaaagga aactictaga atgtacatag 825
 Gly Thr Lys Ser Thr Thr Val *
 255

tctgtacaat aaatacaaca gaaaattgca cagtcaattt ctgttggttg g 876

Figure 22c

SEQ ID No. 04

```

Met Asn Lys Leu Lys Ser Ser Gln Lys Asp Lys Val Arg Gln Phe Met
 1           5           10           15

Ile Phe Thr Gln Ser Ser Glu Lys Thr Ala Val Ser Cys Leu Ser Gln
 20           25           30

Asn Asp Trp Lys Leu Asp Val Ala Thr Asp Asn Phe Phe Gln Asn Pro
 35           40           45

Glu Leu Tyr Ile Arg Glu Ser Val Lys Gly Ser Leu Asp Arg Lys Lys
 50           55           60

Leu Glu Gln Leu Tyr Asn Arg Tyr Lys Asp Pro Gln Asp Glu Asn Lys
 65           70           75

Ile Gly Ile Asp Gly Ile Gln Gln Phe Cys Asp Asp Leu Ala Leu Asp
 80           85           90

Pro Ala Ser Ile Ser Val Leu Ile Ile Ala Trp Lys Phe Arg Ala Ala
 95           100          105          110

Thr Gln Cys Glu Phe Ser Lys Gln Glu Phe Met Asp Gly Met Thr Glu
 115          120          125

Leu Gly Cys Asp Ser Thr Glu Lys Leu Lys Ala Gln Ile Pro Lys Met
 130          135          140

Glu Gln Glu Leu Lys Glu Pro Gly Arg Phe Lys Asp Phe Tyr Gln Phe
 145          150          155          160

Thr Phe Asn Phe Ala Lys Asn Pro Gly Gln Lys Gly Leu Asp Leu Glu
 165          170          175

Met Ala Ile Ala Tyr Trp Asn Leu Val Leu Asn Gly Arg Phe Arg Leu

Leu Asp Leu Trp Asn Lys Phe Leu Leu Glu His His Lys Arg Ser Ile
 185          190          195          200          205

Pro Lys Asp Thr Trp Asn Leu Leu Leu Asp Phe Ser Thr Met Ile Ala
 210          215          220

Asp Asp Met Ser Asn Tyr Asp Glu Glu Gly Ala Trp Pro Val Leu Ile
 225          230          235          240

Asp Asp Phe Val Glu Phe Ala Arg Pro Gln Ile Ala Gly Thr Lys Ser
 245          250          255

Thr Thr Val

```

Figure 22d

(A) 339isiRNA (SEQ ID No. 05)

gatcCCCGTTCAGAGCAGCAACACAGTTCAAGAGACTGTGTTGCTGCTCTGAA
CTTTTGGAAA

(B) ConisiRNA (SEQ ID No.06)

gatcCCCCGTCTACCTACACTCCCTCTTCAAGAGAGAGGGAGTGTAGGTAGAC
GTTTTTA

Figure 23

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